



SEQUENCE LISTING

<110> Vannuza, Pascal
<111> Gafa, Jean-Luc

<120> GENETIC SEQs.,...METHODS & DEVICES FOR
ID. OF STAPHYLOCOCCI STRAINS

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<130> DECLE27.001APC

<140> 09/509,234

<141> 2000-09-25

<150> EP 97870146.4

<151> 1997-09-26

<160> 64

<170> FastSEQ for Windows Version 4.0

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<212> DNA

<213> Staphylococcus femA Consensus Sequence

<220>

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<223> n=any nucleotide

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ngannnnatg ncnnanagn c atttnacnca nannnnngnn nantangan tnaannttgc 120
nnannnnnnn gannncncann tagtnggnat naanaanaan nataangang tnattgcngc 180
ntgnnntntn acngcngtnc cngtnatgaa antntnaan tantttatt cnaanngngg 240
nccngtnatn gatttnana annnaganct ngtncantnn ttctttaang antnnnnnaa 300
ntatntnaaa nannnnntn nnntatannt nnnnntngan ccntanntnn cntatcaata 360
nnnnnaatcat gangngann tnnnngnnaa tgcnggnan gattggntnt tngatnannt 420
nnnnnnnnntn ggntntnanc annnnggntt nnnnannggn tttgancnn tnnnncaaat 480
nngntnnccan tcngtnntn atttannnnn naaaannncn nanganntnn tnaannnnat 540
ggatngnnntn ngnaanngna anacnaaaaa agttnanaan aatggngtta aagtnnnntt 600
nntnnnnnaa gananntnc cnatnttng ntcattnatg gangatacnn cngannchaa 660
ngnnttnnn gatngngang annnnttnta ntanaannngn tnnnnnnatt nnaaaganng 720
ngtnntngtn ccnnntngcnt atatnnantt tgatgantan nttnnnngaa tnnannnnng 780
nngnnnnnn ntnantaaag annnnaanaa agcnntnaan ganatngana aangnccnga 840
naanaaaaaan gcnnnnaana annnnnnnnaa nntnnaanan caantnnnng cnaannanca 900
aaanntnnan gangnnnnnn nnntnnaann nnancatggn aangaattac cnatntcngc 960
ngnntncttn ntnatnaatc cnntngaaat ngntntantan gcnggtggna cntcnaatnn 1020
ntnnngncan ttngcngna gntatgcnn ncaatggnnn atgattaant atgcnnntnna 1080
ncatnnnatn nanngtana atttntatgg nnttagnggt nantttanng angangcnga 1140
agatgnnggn gtnntnaant taaaaaangg ntnnnatgcn ganntnnnng antangttgg 1200
nganttnntn aaaccnatna anaancnn ntannnnnnn tatannncan taaaaaannt 1260
nnannnnnann nnnnnntann nannnnnnna nnnnnnnnn nnnnnnatga aatttacaga 1320

gttaannn

<210> 2
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<220>
 <223> Primer

<221> misc_feature
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 anaatgaantt ttacnaattt nacngcnana gantt

35

<210> 3
 <211> 20
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 <213> Artificial Sequence

<220>
 <223> Primer

<400> 3
 taatgaagtt tacaaaattt

20

<210> 4
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<221> misc_feature
 <222> 14
 <223> n= any nucleotide

<400> 4
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<210> 5
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 <212> DNA
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<220>
 <223> Primer

<221> misc_feature
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 <223> n= any nucleotide

<400> 5
atgncnnana gncattnac ncana

25

<210> 6
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<400> 6
tgccatatacg tcatttacgc

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<210> 7
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<222> (1) ... (37)
<223> n= any nucleotide

<400> 7
tagtnggnat naanaanaan nataangang tnattgc

37

<210> 8
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<221> misc_feature
<222> (1) ... (35)
<223> n= any nucleotide

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gtncnctna tgaaanttt naantantt tattc

35

<210> 9
<211> 18
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<213> Artificial Sequence

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<223> Primer

<221> misc_feature
<222> (1) ... (18)
<223> n= any nucleotide

<400> 9
aatgcnggn angattgg 18

<210> 10
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<223> Primer

<221> misc_feature
<222> (1)...(43)
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<210> 11
<211> 18
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<213> Artificial Sequence

<220>
<223> Primer

<400> 11
aaaaagttca aaaaatgg 18

<210> 12
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 12
aaaaagtaca aaaaatgg 18

<210> 13
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<213> Artificial Sequence

<220>
<223> Primer

<221> misc_feature
<222> (1)...(40)
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<400> 13
aagangannt nccnatnttn ngntcattna tggangatac 40

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<221> misc_feature
<222> (1)...(20)
<223> n= any nucleotide

<400> 14
tatatnnant ttgatganta

20

<210> 15
<211> 32
<212> DNA
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<222> (1)...(32)
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<400> 15
aanganatng anaaaangncc nganaanaaa aa

32

<210> 16
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<212> DNA
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<220>
<223> Primer

<400> 16
aaagatattg aaaaacgaa

18

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 17
aaagatattg aaaagagacc

20

<210> 18
<211> 18

<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 18
aaagatatcg agaaagac

18

<210> 19
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 19
aaagacatcg acaagcgt

18

<210> 20
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<221> misc_feature
<222> (1) ... (22)
<223> n= any nucleotide

<400> 20
ancatggnaa ngaattacn at

22

<210> 21
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 21
gaacatggta atgaattac

19

<210> 22
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<221> misc_feature

<222> (1) ... (32)
<223> n= any nucleotide

<400> 22
aatccntntg aagtngtnta ntangcnggt gg

32

<210> 23
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<221> misc_feature
<222> (1) ... (35)
<223> n= any nucleotide

<400> 23
agntatgcnn tncaatggnn natgattna tatgc

35

<210> 24
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<221> misc_feature
<222> (1) ... (44)
<223> n= any nucleotide

<400> 24
tttanngang angcngaaga tgnngngtn nttaanttna aaaa

44

<210> 25
<211> 20
<212> DNA
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<220>
<223> Primer

<400> 25
tttactgaag atgctgaaga

20

<210> 26
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<220>
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<221> misc_feature
<222> (1)...(20)
<223> n= any nucleotide

<400> 26
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<210> 27
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 27
gttggtgact ttattaaacc

20

<210> 28
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 28
atgaaattta cagagttaa

19

<210> 29
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 29
acagcagatg acatcatt

18

<210> 30
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 30
taatgaaaga aatgtgctta

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<210> 31
<211> 19
<212> DNA
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<220>
<223> Primer

<400> 31 19
acacaacttc aattagaac

<210> 32
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 32 17
agtattagca aatgcgg

<210> 33
<211> 17
<212> DNA
<213> Artificial Sequence

D |
<220>
<223> Primer

<400> 33 17
atgcatattt tccgtaa

<210> 34
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 34 17
cagcagatga catcatt

<210> 35
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 35 23
catctaaaga tatattaaat gga

<210> 36
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 36
agtattagca aatgcgggtc ac

22

<210> 37
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 37
caacacaact tcaattagaa

20

<210> 38
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 38
tggctatcgt gtcacaatcg

20

<210> 39
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 39
ctggaacttg ttgagcagag

20

<210> 40
<211> 1305
<212> DNA
<213> Staphylococcus haemolyticus femA

<220>
<221> CDS
<222> (4) ... (1266)

<400> 40
ata atg aag ttt aca aat tta aca gct aca gag ttt ggc aat tat aca 48
Met Lys Phe Thr Asn Leu Thr Ala Thr Glu Phe Gly Asn Tyr Thr
1 5 10 15

gat aag atg cca tat agt cat ttc aca caa atg act gaa aac tat gag 96

Asp Lys Met Pro Tyr Ser His Phe Thr Gln Met Thr Glu Asn Tyr Glu
 20 25 30
 atg aaa gtt gca aat aaa aca gaa act cac tta gtt ggt ata aaa aat 144
 Met Lys Val Ala Asn Lys Thr Glu Thr His Leu Val Gly Ile Lys Asn
 35 40 45
 aaa gat aat gag gtt att gca gcc tgc atg ttg aca gca gta cca gtc 192
 Lys Asp Asn Glu Val Ile Ala Ala Cys Met Leu Thr Ala Val Pro Val
 50 55 60
 atg aaa ttt ttt aag tac ttt tat tct aac cga gga cct gta att gat 240
 Met Lys Phe Phe Lys Tyr Phe Tyr Ser Asn Arg Gly Pro Val Ile Asp
 65 70 75
 tat gat aat aga gag ctt gtt cac ttt ttc ttt aat gag tta aca aag 288
 Tyr Asp Asn Arg Glu Leu Val His Phe Phe Asn Glu Leu Thr Lys
 80 85 90 95
 tat tta aaa cag cat aat tgt cta tat gtt cga gtt gac cct tat tta 336
 Tyr Leu Lys Gln His Asn Cys Leu Tyr Val Arg Val Asp Pro Tyr Leu
 100 105 110
 cca tat caa tat tta aat cat gat ggt gaa att aca ggt aat gct ggt 384
 Pro Tyr Gln Tyr Leu Asn His Asp Gly Glu Ile Thr Gly Asn Ala Gly
 115 120 125
 aat gat tgg ttc ttt gat aag atg aag cat ctc gga ttt gaa cat gaa 432
 Asn Asp Trp Phe Phe Asp Lys Met Lys His Leu Gly Phe Glu His Glu
 130 135 140
 ggc ttt act aaa ggt ttt gat ccg att aaa caa atc cga tat cat tct 480
 Gly Phe Thr Lys Gly Phe Asp Pro Ile Lys Gln Ile Arg Tyr His Ser
 145 150 155
 gtt tta gat tta aaa aat aaa aca tct aaa gat ata tta aat gga atg 528
 Val Leu Asp Leu Lys Asn Lys Thr Ser Lys Asp Ile Leu Asn Gly Met
 160 165 170 175
 gat agt cta cgt aaa cgt aat act aaa aaa gtt caa aaa aat ggt gtg 576
 Asp Ser Leu Arg Lys Arg Asn Thr Lys Lys Val Gln Lys Asn Gly Val
 180 185 190
 aaa gtt aag ttc tta tca gaa gaa gaa ctt cca atc ttc cgt tca ttt 624
 Lys Val Lys Phe Leu Ser Glu Glu Leu Pro Ile Phe Arg Ser Phe
 195 200 205
 atg gaa gat aca acc gaa acg aaa gaa ttc caa gat aga gat gat agt 672
 Met Glu Asp Thr Thr Glu Thr Lys Glu Phe Gln Asp Arg Asp Ser
 210 215 220
 ttc tat tat aat cgc tat aga cat ttc aaa gat cac gtg ctt gta cca 720
 Phe Tyr Tyr Asn Arg Tyr Arg His Phe Lys Asp His Val Leu Val Pro
 225 230 235

cta gct tat att aag ttt gat gag tac atc gaa gaa tta caa aat gaa 768
 Leu Ala Tyr Ile Lys Phe Asp Glu Tyr Ile Glu Glu Leu Gln Asn Glu
 240 245 250 255
 cgt gaa act tta aat aaa gat gtt aat aaa gct tta aaa gat att gaa 816
 Arg Glu Thr Leu Asn Lys Asp Val Asn Lys Ala Leu Lys Asp Ile Glu
 260 265 270
 aaa cga cca gac aat aaa aag gca ttt aat aaa aaa gaa aat ctt gaa 864
 Lys Arg Pro Asp Asn Lys Lys Ala Phe Asn Lys Lys Glu Asn Leu Glu
 275 280 285
 aaa caa tta gat gcc aat caa caa aaa tta gac gag gct aaa aaa tta 912
 Lys Gln Leu Asp Ala Asn Gln Gln Lys Leu Asp Glu Ala Lys Lys Leu
 290 295 300
 caa gcc gaa cat ggt aat gaa tta cca att tca gca ggt ttc ttc ttt 960
 Gln Ala Glu His Gly Asn Glu Leu Pro Ile Ser Ala Gly Phe Phe Phe
 305 310 315
 att aat cca ttt gaa gtt gtt tat tat gca ggt gga act tct aat aaa 1008
 Ile Asn Pro Phe Glu Val Val Tyr Tyr Ala Gly Gly Thr Ser Asn Lys
 320 325 330 335
 tat aga cat ttt gca ggc agt tat gct att caa tgg aca atg att aac 1056
 Tyr Arg His Phe Ala Gly Ser Tyr Ala Ile Gln Trp Thr Met Ile Asn
 340 345 350
 tat gca att gat cat ggt att gat aga tac aat ttc tat ggt att agc 1104
 Tyr Ala Ile Asp His Gly Ile Asp Arg Tyr Asn Phe Tyr Gly Ile Ser
 355 360 365
 ggt aat ttt agt gaa gac gct gaa gat gtt gga gtc att aaa ttt aaa 1152
 Gly Asn Phe Ser Glu Asp Ala Glu Asp Val Gly Val Ile Lys Phe Lys
 370 375 380
 aaa ggt ttc aat gca gac gta att gag tat gtt gga gac ttt gtg aaa 1200
 Lys Gly Phe Asn Ala Asp Val Ile Glu Tyr Val Gly Asp Phe Val Lys
 385 390 395
 cct att aac aaa cct ttg tat tca gtg tat aag aca ctc aaa aag att 1248
 Pro Ile Asn Lys Pro Leu Tyr Ser Val Tyr Lys Thr Leu Lys Lys Ile
 400 405 410 415
 aaa aaa aga ttt aat taa agagggaaat agacgaatat gaaatttaca 1296
 Lys Lys Arg Phe Asn *
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 gagttaaac 1305

<210> 41
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 <212> PRT
 <213> *Staphylococcus haemolyticus* femA

<400> 41
 Met Lys Phe Thr Asn Leu Thr Ala Thr Glu Phe Gly Asn Tyr Thr Asp
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 Lys Met Pro Tyr Ser His Phe Thr Gln Met Thr Glu Asn Tyr Glu Met
 20 25 30
 Lys Val Ala Asn Lys Thr Glu Thr His Leu Val Gly Ile Lys Asn Lys
 35 40 45
 Asp Asn Glu Val Ile Ala Ala Cys Met Leu Thr Ala Val Pro Val Met
 50 55 60
 Lys Phe Phe Lys Tyr Phe Tyr Ser Asn Arg Gly Pro Val Ile Asp Tyr
 65 70 75 80
 Asp Asn Arg Glu Leu Val His Phe Phe Asn Glu Leu Thr Lys Tyr
 85 90 95
 Leu Lys Gln His Asn Cys Leu Tyr Val Arg Val Asp Pro Tyr Leu Pro
 100 105 110
 Tyr Gln Tyr Leu Asn His Asp Gly Glu Ile Thr Gly Asn Ala Gly Asn
 115 120 125
 Asp Trp Phe Phe Asp Lys Met Lys His Leu Gly Phe Glu His Glu Gly
 130 135 140
 Phe Thr Lys Gly Phe Asp Pro Ile Lys Gln Ile Arg Tyr His Ser Val
 145 150 155 160
 Leu Asp Leu Lys Asn Lys Thr Ser Lys Asp Ile Leu Asn Gly Met Asp
 165 170 175
 Ser Leu Arg Lys Arg Asn Thr Lys Lys Val Gln Lys Asn Gly Val Lys
 180 185 190
 Val Lys Phe Leu Ser Glu Glu Leu Pro Ile Phe Arg Ser Phe Met
 195 200 205
 Glu Asp Thr Thr Glu Thr Lys Glu Phe Gln Asp Arg Asp Asp Ser Phe
 210 215 220
 Tyr Tyr Asn Arg Tyr Arg His Phe Lys Asp His Val Leu Val Pro Leu
 225 230 235 240
 Ala Tyr Ile Lys Phe Asp Glu Tyr Ile Glu Glu Leu Gln Asn Glu Arg
 245 250 255
 Glu Thr Leu Asn Lys Asp Val Asn Lys Ala Leu Lys Asp Ile Glu Lys
 260 265 270
 Arg Pro Asp Asn Lys Lys Ala Phe Asn Lys Lys Glu Asn Leu Glu Lys
 275 280 285
 Gln Leu Asp Ala Asn Gln Gln Lys Leu Asp Glu Ala Lys Lys Leu Gln
 290 295 300
 Ala Glu His Gly Asn Glu Leu Pro Ile Ser Ala Gly Phe Phe Phe Ile
 305 310 315 320
 Asn Pro Phe Glu Val Val Tyr Tyr Ala Gly Gly Thr Ser Asn Lys Tyr
 325 330 335
 Arg His Phe Ala Gly Ser Tyr Ala Ile Gln Trp Thr Met Ile Asn Tyr
 340 345 350
 Ala Ile Asp His Gly Ile Asp Arg Tyr Asn Phe Tyr Gly Ile Ser Gly
 355 360 365
 Asn Phe Ser Glu Asp Ala Glu Asp Val Gly Val Ile Lys Phe Lys Lys
 370 375 380
 Gly Phe Asn Ala Asp Val Ile Glu Tyr Val Gly Asp Phe Val Lys Pro
 385 390 395 400
 Ile Asn Lys Pro Leu Tyr Ser Val Tyr Lys Thr Leu Lys Lys Ile Lys
 405 410 415
 Lys Arg Phe Asn
 420

<210> 42
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 <212> DNA
 <213> *Staphylococcus lugdunensis* femA

<220>
 <221> CDS
 <222> (1) ... (1242)

<400> 42

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1 5 10 15	

ttt act caa atg aca ggt aac tat aat tta aaa gtt gcc gaa aaa aca

96	
Phe Thr Gln Met Thr Gly Asn Tyr Asn Leu Lys Val Ala Glu Lys Thr	
20 25 30	

gaa aca cat tta gtt ggt gtt aaa aat aat aat aac gaa gta att gca

144	
Glu Thr His Leu Val Gly Val Lys Asn Asn Asn Glu Val Ile Ala	
35 40 45	

gca tgt tta ttg aca gct gta cca gtc atg aag ttt ttt aaa tac ttt

192	
Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Phe Phe Lys Tyr Phe	
50 55 60	

tac agc aat aga ggc cca gtt ata gat tat gct aac caa gaa ctt gta

240	
Tyr Ser Asn Arg Gly Pro Val Ile Asp Tyr Ala Asn Gln Glu Leu Val	
65 70 75 80	

cat ttt ttc ttt aat gag cta act aaa tat tta aaa aag tat aac tgt

288	
His Phe Phe Asn Glu Leu Thr Lys Tyr Leu Lys Lys Tyr Asn Cys	
85 90 95	

ctc tat gtc cgc ata gat cca tac tta cct tat caa tat aga gac cat

336	
Leu Tyr Val Arg Ile Asp Pro Tyr Leu Pro Tyr Gln Tyr Arg Asp His	
100 105 110	

gac ggt aat ata acg gca aat gct ggc aat gat tgg ttt ttc aat aaa

384	
Asp Gly Asn Ile Thr Ala Asn Ala Gly Asn Asp Trp Phe Phe Asn Lys	
115 120 125	

atg gaa caa ctc gga tac cat cat gat ggc ttt aca aca gga ttt gat

432	
Met Glu Gln Leu Gly Tyr His His Asp Gly Phe Thr Thr Gly Phe Asp	
130 135 140	

cca ata tta caa atc aga ttc cat tct att ctt aat tta aag gat aag

480	
Pro Ile Leu Gln Ile Arg Phe His Ser Ile Leu Asn Leu Lys Asp Lys	
145 150 155 160	

aca gct aaa gat gtt tta aat aat atg gat agt tta cgt aaa aga aat

528	
Thr Ala Lys Asp Val Leu Asn Asn Met Asp Ser Leu Arg Lys Arg Asn	
165 170 175	

acc aaa aaa agt tca aaa aat gga gtc aaa gta aag ttc ctt act gaa 576
 Thr Lys Lys Ser Ser Lys Asn Gly Val Lys Val Lys Phe Leu Thr Glu
 180 185 190
 gaa gaa cta cct atc ttt cgt tca ttt atg gag cag acg tca gaa tct 624
 Glu Glu Leu Pro Ile Phe Arg Ser Phe Met Glu Gln Thr Ser Glu Ser
 195 200 205
 aaa gaa ttc tct gat aga gac gac caa ttt tat tac aat cgg ttt aag 672
 Lys Glu Phe Ser Asp Arg Asp Asp Gln Phe Tyr Tyr Asn Arg Phe Lys
 210 215 220
 tac tat aaa gat agg gtg ctt gtg cct cta gca tat tta aaa ttt gat 720
 Tyr Tyr Lys Asp Arg Val Leu Val Pro Leu Ala Tyr Leu Lys Phe Asp
 225 230 235 240
 gaa tat ata gaa gaa cta acg aat gaa cga caa act tta gaa aaa gat 768
 Glu Tyr Ile Glu Glu Leu Thr Asn Glu Arg Gln Thr Leu Glu Lys Asp
 245 250 255
 tta ggc aaa gca ctt aaa gac att gag aaa cga cca gat aac aaa aaa 816
 Leu Gly Lys Ala Leu Lys Asp Ile Glu Lys Arg Pro Asp Asn Lys Lys
 260 265 270
 gct tat aat aaa cga gac aac cta caa caa ctc gat gcc aat caa 864
 Ala Tyr Asn Lys Arg Asp Asn Leu Gln Gln Leu Asp Ala Asn Gln
 275 280 285
 caa aag tta aat gag gct aat cag tta caa gcg gaa cac ggt aat gag 912
 Gln Lys Leu Asn Glu Ala Asn Gln Leu Gln Ala Glu His Gly Asn Glu
 290 295 300
 tta cct atc tct gcc ggt ttc ttt att att aat ccg ttt gaa gtt gta 960
 Leu Pro Ile Ser Ala Gly Phe Phe Ile Ile Asn Pro Phe Glu Val Val
 305 310 315 320
 tac tac gct gga ggt acc gct aat aaa tat cgt cat ttt gca ggt agt 1008
 Tyr Tyr Ala Gly Gly Thr Ala Asn Lys Tyr Arg His Phe Ala Gly Ser
 325 330 335
 tac gcg gtt cag tgg act atg att aac tat gct atc gaa cac ggc ata 1056
 Tyr Ala Val Gln Trp Thr Met Ile Asn Tyr Ala Ile Glu His Gly Ile
 340 345 350
 gac aga tat aat ttc tac ggc att agt gga aac ttc tca gat gat gct 1104
 Asp Arg Tyr Asn Phe Tyr Gly Ile Ser Gly Asn Phe Ser Asp Asp Ala
 355 360 365
 gaa gac gca ggt gtc att cgc ttt aaa aaa ggt tat ggt gca gaa gtg 1152
 Glu Asp Ala Gly Val Ile Arg Phe Lys Lys Gly Tyr Gly Ala Glu Val
 370 375 380
 att gaa tac gtt ggt gat ttt gta aaa cct ata aat aaa cct atg tat 1200
 Ile Glu Tyr Val Gly Asp Phe Val Lys Pro Ile Asn Lys Pro Met Tyr

385

390

395

400

aaa ctt tat tca gtg tta aaa cga att caa aat aag cta tag
 Lys Leu Tyr Ser Val Leu Lys Arg Ile Gln Asn Lys Leu *
 405 410

1242

aggagaatgg attaattatg aaatttacag agtttaac

1280

<210> 43
 <211> 413
 <212> PRT
 <213> *Staphylococcus lugdunensis* femA

<400> 43
 Thr Ala Asn Glu Phe Gly Asp Phe Thr Asp Gln Met Pro Tyr Ser His
 1 5 10 15
 Phe Thr Gln Met Thr Gly Asn Tyr Asn Leu Lys Val Ala Glu Lys Thr
 20 25 30
 Glu Thr His Leu Val Gly Val Lys Asn Asn Asn Glu Val Ile Ala
 35 40 45
 Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Phe Phe Lys Tyr Phe
 50 55 60
 Tyr Ser Asn Arg Gly Pro Val Ile Asp Tyr Ala Asn Gln Glu Leu Val
 65 70 75 80
 His Phe Phe Asn Glu Leu Thr Lys Tyr Leu Lys Lys Tyr Asn Cys
 85 90 95
 Leu Tyr Val Arg Ile Asp Pro Tyr Leu Pro Tyr Gln Tyr Arg Asp His
 100 105 110
 Asp Gly Asn Ile Thr Ala Asn Ala Gly Asn Asp Trp Phe Phe Asn Lys
 115 120 125
 Met Glu Gln Leu Gly Tyr His His Asp Gly Phe Thr Thr Gly Phe Asp
 130 135 140
 Pro Ile Leu Gln Ile Arg Phe His Ser Ile Leu Asn Leu Lys Asp Lys
 145 150 155 160
 Thr Ala Lys Asp Val Leu Asn Asn Met Asp Ser Leu Arg Lys Arg Asn
 165 170 175
 Thr Lys Lys Ser Ser Lys Asn Gly Val Lys Val Lys Phe Leu Thr Glu
 180 185 190
 Glu Glu Leu Pro Ile Phe Arg Ser Phe Met Glu Gln Thr Ser Glu Ser
 195 200 205
 Lys Glu Phe Ser Asp Arg Asp Asp Gln Phe Tyr Tyr Asn Arg Phe Lys
 210 215 220
 Tyr Tyr Lys Asp Arg Val Leu Val Pro Leu Ala Tyr Leu Lys Phe Asp
 225 230 235 240
 Glu Tyr Ile Glu Glu Leu Thr Asn Glu Arg Gln Thr Leu Glu Lys Asp
 245 250 255
 Leu Gly Lys Ala Leu Lys Asp Ile Glu Lys Arg Pro Asp Asn Lys Lys
 260 265 270
 Ala Tyr Asn Lys Arg Asp Asn Leu Gln Gln Leu Asp Ala Asn Gln
 275 280 285
 Gln Lys Leu Asn Glu Ala Asn Gln Leu Gln Ala Glu His Gly Asn Glu
 290 295 300
 Leu Pro Ile Ser Ala Gly Phe Phe Ile Ile Asn Pro Phe Glu Val Val
 305 310 315 320
 Tyr Tyr Ala Gly Gly Thr Ala Asn Lys Tyr Arg His Phe Ala Gly Ser

325	330	335
Tyr Ala Val Gln Trp Thr Met Ile Asn Tyr Ala Ile Glu His Gly Ile		
340	345	350
Asp Arg Tyr Asn Phe Tyr Gly Ile Ser Gly Asn Phe Ser Asp Asp Ala		
355	360	365
Glu Asp Ala Gly Val Ile Arg Phe Lys Lys Gly Tyr Gly Ala Glu Val		
370	375	380
Ile Glu Tyr Val Gly Asp Phe Val Lys Pro Ile Asn Lys Pro Met Tyr		
385	390	395
Lys Leu Tyr Ser Val Leu Lys Arg Ile Gln Asn Lys Leu		
405	410	

<210> 44

<211> 1295

<212> DNA

<213> *Staphylococcus xylosus* femA

<220>

<221> CDS

<222> (1) ... (1245)

<400> 44

acg caa aag agt ttg ggt gca ttt tca gat aaa atg cca aat agc cat	48		
Thr Gln Lys Ser Leu Gly Ala Phe Ser Asp Lys Met Pro Asn Ser His			
1	5	10	15

ttc acg caa atg gta ggg aat tat gaa ttg aaa att gca gaa agt act	96		
Phe Thr Gln Met Val Gly Asn Tyr Glu Leu Lys Ile Ala Glu Ser Thr			
20	25	30	

gaa aca cat tta gta ggt ata aaa aac aat gat aat gaa gtc att gca	144		
Glu Thr His Leu Val Gly Ile Lys Asn Asn Asp Asn Glu Val Ile Ala			
35	40	45	

gct tgt tta tta act gca gta cca gta atg aaa ttc ttt aag tat ttt	192		
Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Phe Phe Lys Tyr Phe			
50	55	60	

tat act aat aga ggt ccg gtt ata gat ttt gaa aat aaa gaa tta gtg	240		
Tyr Thr Asn Arg Gly Pro Val Ile Asp Phe Glu Asn Lys Glu Leu Val			
65	70	75	80

cat tac ttt ttc aat gaa cta tct aaa tat gtg aaa aaa cat aat gcg	288		
His Tyr Phe Asn Glu Leu Ser Lys Tyr Val Lys Lys His Asn Ala			
85	90	95	

ctt tat tta aga gtt gat cct tat tta gca tat caa tac cgt aat cat	336		
Leu Tyr Leu Arg Val Asp Pro Tyr Leu Ala Tyr Gln Tyr Arg Asn His			
100	105	110	

gat ggt gag gta ttg gaa aat gca gga cat gat tgg att ttc gat aaa	384		
Asp Gly Glu Val Leu Glu Asn Ala Gly His Asp Trp Ile Phe Asp Lys			
115	120	125	

atg aag cag ctt gga tat aaa cac caa gga ttt tta act ggt ttc gat 432
 Met Lys Gln Leu Gly Tyr Lys His Gln Gly Phe Leu Thr Gly Phe Asp
 130 135 140

 tca att att caa att agg ttc cac tct gta ctg gat tta gta ggt aaa 480
 Ser Ile Ile Gln Ile Arg Phe His Ser Val Leu Asp Leu Val Gly Lys
 145 150 155 160

 act gct aaa gat gta cta aat ggt atg gat agt tta cgt aaa cgt aat 528
 Thr Ala Lys Asp Val Leu Asn Gly Met Asp Ser Leu Arg Lys Arg Asn
 165 170 175

 act aaa aaa gta caa aaa aat ggc gtg aaa gta agg ttc tta agg gaa 576
 Thr Lys Lys Val Gln Lys Asn Gly Val Lys Val Arg Phe Leu Arg Glu
 180 185 190

 gat gag ttg cca att ttc cgt tca ttc atg gaa gat aca tct gaa act 624
 Asp Glu Leu Pro Ile Phe Arg Ser Phe Met Glu Asp Thr Ser Glu Thr
 195 200 205

 aaa gac ttt gac gat aga gac gat ggc ttt tac tac aat aga tta agg 672
 Lys Asp Phe Asp Asp Arg Asp Gly Phe Tyr Tyr Asn Arg Leu Arg
 210 215 220

 D1
 tat tat aaa gat cgc gta tta gta cct cta gct tat atg gat ttc aat 720
 Tyr Tyr Lys Asp Arg Val Leu Val Pro Leu Ala Tyr Met Asp Phe Asn
 225 230 235 240

 gaa tat att gaa gaa ttg caa gct gaa cgt gag gtg tta agc aaa gat 768
 Glu Tyr Ile Glu Glu Leu Gln Ala Glu Arg Glu Val Leu Ser Lys Asp
 245 250 255

 atc aat aaa gca gta aaa gat atc gag aaa aga cct gaa aat aaa aaa 816
 Ile Asn Lys Ala Val Lys Asp Ile Glu Lys Arg Pro Glu Asn Lys Lys
 260 265 270

 gca tat aat aaa aaa gat aat cta gag aaa caa ctt ata gcg aat caa 864
 Ala Tyr Asn Lys Lys Asp Asn Leu Glu Lys Gln Leu Ile Ala Asn Gln
 275 280 285

 caa aaa att gat gaa gct aaa act cta caa gag aag cat ggt aac gaa 912
 Gln Lys Ile Asp Glu Ala Lys Thr Leu Gln Glu Lys His Gly Asn Glu
 290 295 300

 cta cca atc tca gca gca tat ttc atc att aac cct tat gaa gta gtg 960
 Leu Pro Ile Ser Ala Ala Tyr Phe Ile Ile Asn Pro Tyr Glu Val Val
 305 310 315 320

 tat tat gcg ggt gga acg tca aat gag ttt aga cat ttt gct ggt agt 1008
 Tyr Tyr Ala Gly Gly Thr Ser Asn Glu Phe Arg His Phe Ala Gly Ser
 325 330 335

 tat gcc att caa tgg aag atg att aac tat gct att gac cat aat att 1056
 Tyr Ala Ile Gln Trp Lys Met Ile Asn Tyr Ala Ile Asp His Asn Ile
 340 345 350

gat aga tat aat ttt tat gga att agt ggt cat ttt aca gaa gat gca 1104
 Asp Arg Tyr Asn Phe Tyr Gly Ile Ser Gly His Phe Thr Glu Asp Ala
 355 360 365
 gaa gat gcc ggt gta gtt aaa ttt aaa gga ttt aat gcg gat gta 1152
 Glu Asp Ala Gly Val Val Lys Phe Lys Gly Phe Asn Ala Asp Val
 370 375 380
 gtg gaa tat gtt ggt gat ttt att aaa cca atc aat aaa cca atg tac 1200
 Val Glu Tyr Val Gly Asp Phe Ile Lys Pro Ile Asn Lys Pro Met Tyr
 385 390 395 400
 aaa att tat acg aca tta aag aaa att aaa gat aaa aag aaa taa 1245
 Lys Ile Tyr Thr Leu Lys Ile Lys Asp Lys Lys Lys *
 405 410
 acatthaata gaagggact aagctagaat gaaatttaca gagttaaacc 1295

<210> 45
 <211> 414
 <212> PRT
 <213> *Staphylococcus xylosus* femA

<400> 45
 Thr Gln Lys Ser Leu Gly Ala Phe Ser Asp Lys Met Pro Asn Ser His
 1 5 10 15
 Phe Thr Gln Met Val Gly Asn Tyr Glu Leu Lys Ile Ala Glu Ser Thr
 20 25 30
 Glu Thr His Leu Val Gly Ile Lys Asn Asn Asp Asn Glu Val Ile Ala
 35 40 45
 Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Phe Phe Lys Tyr Phe
 50 55 60
 Tyr Thr Asn Arg Gly Pro Val Ile Asp Phe Glu Asn Lys Glu Leu Val
 65 70 75 80
 His Tyr Phe Asn Glu Leu Ser Lys Tyr Val Lys Lys His Asn Ala
 85 90 95
 Leu Tyr Leu Arg Val Asp Pro Tyr Leu Ala Tyr Gln Tyr Arg Asn His
 100 105 110
 Asp Gly Glu Val Leu Glu Asn Ala Gly His Asp Trp Ile Phe Asp Lys
 115 120 125
 Met Lys Gln Leu Gly Tyr Lys His Gln Gly Phe Leu Thr Gly Phe Asp
 130 135 140
 Ser Ile Ile Gln Ile Arg Phe His Ser Val Leu Asp Leu Val Gly Lys
 145 150 155 160
 Thr Ala Lys Asp Val Leu Asn Gly Met Asp Ser Leu Arg Lys Arg Asn
 165 170 175
 Thr Lys Lys Val Gln Lys Asn Gly Val Lys Val Arg Phe Leu Arg Glu
 180 185 190
 Asp Glu Leu Pro Ile Phe Arg Ser Phe Met Glu Asp Thr Ser Glu Thr
 195 200 205
 Lys Asp Phe Asp Asp Arg Asp Asp Gly Phe Tyr Tyr Asn Arg Leu Arg
 210 215 220
 Tyr Tyr Lys Asp Arg Val Leu Val Pro Leu Ala Tyr Met Asp Phe Asn
 225 230 235 240

Glu Tyr Ile Glu Glu Leu Gln Ala Glu Arg Glu Val Leu Ser Lys Asp
 245 250 255
 Ile Asn Lys Ala Val Lys Asp Ile Glu Lys Arg Pro Glu Asn Lys Lys
 260 265 270
 Ala Tyr Asn Lys Lys Asp Asn Leu Glu Lys Gln Leu Ile Ala Asn Gln
 275 280 285
 Gln Lys Ile Asp Glu Ala Lys Thr Leu Gln Glu Lys His Gly Asn Glu
 290 295 300
 Leu Pro Ile Ser Ala Ala Tyr Phe Ile Ile Asn Pro Tyr Glu Val Val
 305 310 315 320
 Tyr Tyr Ala Gly Gly Thr Ser Asn Glu Phe Arg His Phe Ala Gly Ser
 325 330 335
 Tyr Ala Ile Gln Trp Lys Met Ile Asn Tyr Ala Ile Asp His Asn Ile
 340 345 350
 Asp Arg Tyr Asn Phe Tyr Gly Ile Ser Gly His Phe Thr Glu Asp Ala
 355 360 365
 Glu Asp Ala Gly Val Val Lys Phe Lys Lys Gly Phe Asn Ala Asp Val
 370 375 380
 Val Glu Tyr Val Gly Asp Phe Ile Lys Pro Ile Asn Lys Pro Met Tyr
 385 390 395 400
 Lys Ile Tyr Thr Thr Leu Lys Lys Ile Lys Asp Lys Lys Lys
 405 410

D | <210> 46

<211> 1283

<212> DNA

<213> *Staphylococcus capitis* femA

<220>

<221> CDS

<222> (1)...(1236)

<400> 46

aca gct aaa gaa ttt agt gac ttt act gat caa atg cct tat agc cat 48
 Thr Ala Lys Glu Phe Ser Asp Phe Thr Asp Gln Met Pro Tyr Ser His
 1 5 10 15

ttt act cag atg gaa ggt aat tat gaa ctt aaa gtt gct gaa ggt acg 96
 Phe Thr Gln Met Glu Gly Asn Tyr Glu Leu Lys Val Ala Glu Gly Thr
 20 25 30

gat tca cat ctc gta gga att aaa aat aat gac aac caa gtg att gca 144
 Asp Ser His Leu Val Gly Ile Lys Asn Asp Asn Gln Val Ile Ala
 35 40 45

gca tgt tta tta act gct gta cct gta atg aaa att ttt aaa tat ttt 192
 Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Ile Phe Lys Tyr Phe
 50 55 60

tac tca aat cgc ggg cca gtg att gat tat gat aat aaa gag ctt gtt 240
 Tyr Ser Asn Arg Gly Pro Val Ile Asp Tyr Asp Asn Lys Glu Leu Val
 65 70 75 80

cac ttt ttc ttt aat gaa tta agt aaa tat gta aaa aag cat aat tgt 288

His	Phe	Phe	Asn	Glu	Leu	Ser	Lys	Tyr	Val	Lys	Lys	His	Asn	Cys	
85							90					95			
ctt tat cta aga gtt gac cct tat ctt cct tat caa tac tta aat cat														336	
Leu	Tyr	Leu	Arg	Val	Asp	Pro	Tyr	Leu	Pro	Tyr	Gln	Tyr	Leu	Asn	His
100				105					110						
gac ggt gaa att att gga aat gct ggc cat gat tgg ttt ttc aat aag														384	
Asp	Gly	Glu	Ile	Ile	Gly	Asn	Ala	Gly	His	Asp	Trp	Phe	Phe	Asn	Lys
115				120					125						
atg gaa gaa tta gga ttt gaa cat gaa ggc ttt cat aaa ggc ttc cat														432	
Met	Glu	Glu	Leu	Gly	Phe	Glu	His	Glu	Gly	Phe	His	Lys	Gly	Phe	His
130				135					140						
cct atc tta caa gta aga tat cat tca gtt tta gat tta aaa gat aaa														480	
Pro	Ile	Leu	Gln	Val	Arg	Tyr	His	Ser	Val	Leu	Asp	Leu	Lys	Asp	Lys
145				150					155			160			
acg gct aaa gat gta ctc aaa gga atg gat agt tta aga aag cgt aat														528	
Thr	Ala	Lys	Asp	Val	Leu	Lys	Gly	Met	Asp	Ser	Leu	Arg	Lys	Arg	Asn
165				170					175						
act aag aaa gta caa aaa aat ggt gtc aaa gtc cgt ttc cta tcc gaa														576	
Thr	Lys	Lys	Val	Gln	Lys	Asn	Gly	Val	Lys	Val	Arg	Phe	Leu	Ser	Glu
180				185					190						
gat gaa tta cct atc ttt aga tca ttt atg gaa gat act aca gaa acg														624	
Asp	Glu	Leu	Pro	Ile	Phe	Arg	Ser	Phe	Met	Glu	Asp	Thr	Thr	Glu	Thr
195				200					205						
aaa gag ttc gcc gat aga gat gat agt ttc tat tat aat cga tta aaa														672	
Lys	Glu	Phe	Ala	Asp	Arg	Asp	Asp	Ser	Phe	Tyr	Tyr	Asn	Arg	Leu	Lys
210				215					220						
tac ttt aaa gat aga gta tta gta cca tta gca tat gtt gac ttc gat														720	
Tyr	Phe	Lys	Asp	Arg	Val	Leu	Val	Pro	Leu	Ala	Tyr	Val	Asp	Phe	Asp
225				230					235			240			
gag tat att gaa gaa ctt aat aat gaa aga gat gtt ctt aat aaa gat														768	
Glu	Tyr	Ile	Glu	Glu	Leu	Asn	Asn	Glu	Arg	Asp	Val	Leu	Asn	Lys	Asp
245				250					255						
tta aat aag gcg ctc aaa gat att gag aag aga cct gat aat aag aaa														816	
Leu	Asn	Lys	Ala	Leu	Lys	Asp	Ile	Glu	Lys	Arg	Pro	Asp	Asn	Lys	Lys
260				265					270						
gct tat aac aaa aga gat aat ctt caa caa caa tta gat gca aat caa														864	
Ala	Tyr	Asn	Lys	Arg	Asp	Asn	Leu	Gln	Gln	Gln	Leu	Asp	Ala	Asn	Gln
275				280					285						
caa aaa att gat gaa gct aaa aac tta caa caa gaa cat ggt aat gaa														912	
Gln	Lys	Ile	Asp	Glu	Ala	Lys	Asn	Leu	Gln	Gln	Glu	His	Gly	Asn	Glu
290				295					300						

tta cct att tca gct gga tat ttc ttc att aat ccg ttt gaa gtt gtt 960
 Leu Pro Ile Ser Ala Gly Tyr Phe Phe Ile Asn Pro Phe Glu Val Val
 305 310 315 320

 tat tac gca ggt ggc aca tcg aat cgt tat cgt cac tat gcc gga agt 1008
 Tyr Tyr Ala Gly Gly Thr Ser Asn Arg Tyr Arg His Tyr Ala Gly Ser
 325 330 335

 tat gca att caa tgg aaa atg ata aac tat gct tta gaa cat gga att 1056
 Tyr Ala Ile Gln Trp Lys Met Ile Asn Tyr Ala Leu Glu His Gly Ile
 340 345 350

 aac cgt tat aat ttt tat gga gtt agt ggg gac ttc agt gaa gac gct 1104
 Asn Arg Tyr Asn Phe Tyr Gly Val Ser Gly Asp Phe Ser Glu Asp Ala
 355 360 365

 gaa gat gta gga gta att aag ttc aaa aaa ggc tat aat gct gat gtt 1152
 Glu Asp Val Gly Val Ile Lys Phe Lys Lys Gly Tyr Asn Ala Asp Val
 370 375 380

 att gaa tat gta ggt gat ttt atc aag cca atc aat aaa cct atg tat 1200
 Ile Glu Tyr Val Gly Asp Phe Ile Lys Pro Ile Asn Lys Pro Met Tyr
 385 390 395 400

 D | gca atc tat aac gca ctt aaa aag tta aag aaa tag attttttac 1246
 Ala Ile Tyr Asn Ala Leu Lys Lys Leu Lys Lys *
 405 410

 caacccaatt atctaattat gaaatttaca gagttaa 1283

 <210> 47
 <211> 411
 <212> PRT
 <213> *Staphylococcus capitis* femA

 <400> 47
 Thr Ala Lys Glu Phe Ser Asp Phe Thr Asp Gln Met Pro Tyr Ser His
 1 5 10 15
 Phe Thr Gln Met Glu Gly Asn Tyr Glu Leu Lys Val Ala Glu Gly Thr
 20 25 30
 Asp Ser His Leu Val Gly Ile Lys Asn Asn Asp Asn Gln Val Ile Ala
 35 40 45
 Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Ile Phe Lys Tyr Phe
 50 55 60
 Tyr Ser Asn Arg Gly Pro Val Ile Asp Tyr Asp Asn Lys Glu Leu Val
 65 70 75 80
 His Phe Phe Phe Asn Glu Leu Ser Lys Tyr Val Lys Lys His Asn Cys
 85 90 95
 Leu Tyr Leu Arg Val Asp Pro Tyr Leu Pro Tyr Gln Tyr Leu Asn His
 100 105 110
 Asp Gly Glu Ile Ile Gly Asn Ala Gly His Asp Trp Phe Phe Asn Lys
 115 120 125
 Met Glu Glu Leu Gly Phe Glu His Glu Gly Phe His Lys Gly Phe His
 130 135 140
 Pro Ile Leu Gln Val Arg Tyr His Ser Val Leu Asp Leu Lys Asp Lys

145	150	155	160
Thr Ala Lys Asp Val Leu Lys Gly Met Asp Ser Leu Arg Lys Arg Asn			
165	170	175	
Thr Lys Lys Val Gln Lys Asn Gly Val Lys Val Arg Phe Leu Ser Glu			
180	185	190	
Asp Glu Leu Pro Ile Phe Arg Ser Phe Met Glu Asp Thr Thr Glu Thr			
195	200	205	
Lys Glu Phe Ala Asp Arg Asp Asp Ser Phe Tyr Tyr Asn Arg Leu Lys			
210	215	220	
Tyr Phe Lys Asp Arg Val Leu Val Pro Leu Ala Tyr Val Asp Phe Asp			
225	230	235	240
Glu Tyr Ile Glu Glu Leu Asn Asn Glu Arg Asp Val Leu Asn Lys Asp			
245	250	255	
Leu Asn Lys Ala Leu Lys Asp Ile Glu Lys Arg Pro Asp Asn Lys Lys			
260	265	270	
Ala Tyr Asn Lys Arg Asp Asn Leu Gln Gln Gln Leu Asp Ala Asn Gln			
275	280	285	
Gln Lys Ile Asp Glu Ala Lys Asn Leu Gln Gln Glu His Gly Asn Glu			
290	295	300	
Leu Pro Ile Ser Ala Gly Tyr Phe Phe Ile Asn Pro Phe Glu Val Val			
305	310	315	320
Tyr Tyr Ala Gly Gly Thr Ser Asn Arg Tyr Arg His Tyr Ala Gly Ser			
325	330	335	
Tyr Ala Ile Gln Trp Lys Met Ile Asn Tyr Ala Leu Glu His Gly Ile			
340	345	350	
Asn Arg Tyr Asn Phe Tyr Gly Val Ser Gly Asp Phe Ser Glu Asp Ala			
355	360	365	
Glu Asp Val Gly Val Ile Lys Phe Lys Lys Gly Tyr Asn Ala Asp Val			
370	375	380	
Ile Glu Tyr Val Gly Asp Phe Ile Lys Pro Ile Asn Lys Pro Met Tyr			
385	390	395	400
Ala Ile Tyr Asn Ala Leu Lys Lys Leu Lys Lys			
405	410		

<210> 48
<211> 1297
<212> DNA
<213> *Staphylococcus schleiferi* femA

<220>
<221> CDS
<222> (1) ... (1248)

<400> 48 acg acg gct gaa ttt ggt gcg ttt aca gat caa atg cca tat agc cat 48
Thr Thr Ala Glu Phe Gly Ala Phe Thr Asp Gln Met Pro Tyr Ser His
1 5 10 15

ttc acg caa atg gta ggg aac tat gaa tta aag gtt gct gaa ggt gtt 96
 Phe Thr Gln Met Val Gly Asn Tyr Glu Leu Lys Val Ala Glu Gly Val
 20 25 30

gaa aca cat ctt gtc ggc att aaa gat aac aac aat aac gta cta gca 144
Glu Thr His Leu Val Gly Ile Lys Asp Asn Asn Asn Asn Val Leu Ala

gca tgt tta ctg aca gca gtg cca gta atg aag ttt ttt aaa tat ttt 192
 Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Phe Phe Lys Tyr Phe
 50 55 60

tat tca aac cgc gga cca gtc atg gac tac gaa aat aaa gag ctc gtt 240
 Tyr Ser Asn Arg Gly Pro Val Met Asp Tyr Glu Asn Lys Glu Leu Val
 65 70 75 80

cat ttc ttt ttt aat gaa ctt tca aaa tat gtt aag aaa tat cac gca 288
 His Phe Phe Asn Glu Leu Ser Lys Tyr Val Lys Lys Tyr His Ala
 85 90 95

ttg tat ttg aga gta gac cct tat tta cca atg tta aag cga aac cat 336
 Leu Tyr Leu Arg Val Asp Pro Tyr Leu Pro Met Leu Lys Arg Asn His
 100 105 110

gat ggt gaa gtg att gaa aga tac ggc agt gac tgg ttt ttt gat aaa 384
 Asp Gly Glu Val Ile Glu Arg Tyr Gly Ser Asp Trp Phe Phe Asp Lys
 115 120 125

atg gct gaa tta aac ttt gaa cat gaa ggt ttc aca act ggg ttt gat 432
 Met Ala Glu Leu Asn Phe Glu His Gly Phe Thr Thr Gly Phe Asp
 130 135 140

aca ata agg caa att cgt ttt cat tct gtg ctc gat gtt gaa aat aaa 480
 Thr Ile Arg Gln Ile Arg Phe His Ser Val Leu Asp Val Glu Asn Lys
 145 150 155 160

aca tca aaa gac atc tta aat caa atg gat aat tta agg aaa aga aat 528
 Thr Ser Lys Asp Ile Leu Asn Gln Met Asp Asn Leu Arg Lys Arg Asn
 165 170 175

acg aaa aaa gta cag aaa aat ggt gtg aaa gtc cgc tat cta aac gaa 576
 Thr Lys Lys Val Gln Lys Asn Gly Val Lys Val Arg Tyr Leu Asn Glu
 180 185 190

gat gaa tta cat att ttc cgt tcg ttt atg gaa gat aca tct gaa aca 624
 Asp Glu Leu His Ile Phe Arg Ser Phe Met Glu Asp Thr Ser Glu Thr
 195 200 205

aaa gat ttt gta gat aga gat gac gat ttt tat tat cat cgt atg aaa 672
 Lys Asp Phe Val Asp Arg Asp Asp Phe Tyr Tyr His Arg Met Lys
 210 215 220

tac tat aaa gat cgt gtc cgc gta cca cta gcg tat att gat ttt aat 720
 Tyr Tyr Lys Asp Arg Val Arg Val Pro Leu Ala Tyr Ile Asp Phe Asn
 225 230 235 240

gca tat tta gca gag ctc aac act gaa gcg caa gac ttt aaa aaa gaa 768
 Ala Tyr Leu Ala Glu Leu Asn Thr Glu Ala Gln Asp Phe Lys Lys Glu
 245 250 255

att gca aaa gca gat aaa gac atc gac aag cgt cct gaa aat cag aaa 816

Ile Ala Lys Ala Asp Lys Asp Ile Asp Lys Arg Pro Glu Asn Gln Lys
 260 265 270

gcc ata aat aaa aag aaa aat tta gag caa caa cta gaa gcg aat caa 864
 Ala Ile Asn Lys Lys Asn Leu Glu Gln Gln Leu Glu Ala Asn Gln
 275 280 285

gct aaa ata aaa gaa gca gaa aca ttg caa ctt aaa cac ggt gac aca 912
 Ala Lys Ile Lys Glu Ala Glu Thr Leu Gln Leu Lys His Gly Asp Thr
 290 295 300

tta ccg att tcg gct gga ttc ttt att att aat cca ttt gag gtt gtt 960
 Leu Pro Ile Ser Ala Gly Phe Phe Ile Ile Asn Pro Phe Glu Val Val
 305 310 315 320

tat tat gca ggc ggc aca gca aac gaa ttt cgt cat ttt gct gga agc 1008
 Tyr Tyr Ala Gly Gly Thr Ala Asn Glu Phe Arg His Phe Ala Gly Ser
 325 330 335

tac gca gtg caa tgg gaa atg att aat tat gcg att gat tat caa att 1056
 Tyr Ala Val Gln Trp Glu Met Ile Asn Tyr Ala Ile Asp Tyr Gln Ile
 340 345 350

cca aga tat aac ttt tat ggc att agt ggt gat ttt tca gaa gat gca 1104
 Pro Arg Tyr Asn Phe Tyr Gly Ile Ser Gly Asp Phe Ser Glu Asp Ala
 355 360 365

gaa gat gca ggt gtg ata aaa ttt aaa aaa ggc tat aat gca gaa gta 1152
 Glu Asp Ala Gly Val Ile Lys Phe Lys Lys Gly Tyr Asn Ala Glu Val
 370 375 380

ata gaa tat gtc ggt gat ttt att aag cct ata aac aaa cct gcc tat 1200
 Ile Glu Tyr Val Gly Asp Phe Ile Lys Pro Ile Asn Lys Pro Ala Tyr
 385 390 395 400

aca gtc tac tta aaa tta aag caa tta aaa gac aag ata aaa aga taa 1248
 Thr Val Tyr Leu Lys Leu Lys Gln Leu Lys Asp Lys Ile Lys Arg *
 405 410 415

gatatacgaa agagaagggg atttatttgt atgaaattta cagagttaa 1297

<210> 49
 <211> 415
 <212> PRT
 <213> *Staphylococcus schleiferi* femA

<400> 49
 Thr Thr Ala Glu Phe Gly Ala Phe Thr Asp Gln Met Pro Tyr Ser His
 1 5 10 15
 Phe Thr Gln Met Val Gly Asn Tyr Glu Leu Lys Val Ala Glu Gly Val
 20 25 30
 Glu Thr His Leu Val Gly Ile Lys Asp Asn Asn Asn Val Leu Ala
 35 40 45
 Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Phe Phe Lys Tyr Phe
 50 55 60

Tyr Ser Asn Arg Gly Pro Val Met Asp Tyr Glu Asn Lys Glu Leu Val
 65 70 75 80
 His Phe Phe Asn Glu Leu Ser Lys Tyr Val Lys Lys Tyr His Ala
 85 90 95
 Leu Tyr Leu Arg Val Asp Pro Tyr Leu Pro Met Leu Lys Arg Asn His
 100 105 110
 Asp Gly Glu Val Ile Glu Arg Tyr Gly Ser Asp Trp Phe Phe Asp Lys
 115 120 125
 Met Ala Glu Leu Asn Phe Glu His Glu Gly Phe Thr Thr Gly Phe Asp
 130 135 140
 Thr Ile Arg Gln Ile Arg Phe His Ser Val Leu Asp Val Glu Asn Lys
 145 150 155 160
 Thr Ser Lys Asp Ile Leu Asn Gln Met Asp Asn Leu Arg Lys Arg Asn
 165 170 175
 Thr Lys Lys Val Gln Lys Asn Gly Val Lys Val Arg Tyr Leu Asn Glu
 180 185 190
 Asp Glu Leu His Ile Phe Arg Ser Phe Met Glu Asp Thr Ser Glu Thr
 195 200 205
 Lys Asp Phe Val Asp Arg Asp Asp Phe Tyr Tyr His Arg Met Lys
 210 215 220
 Tyr Tyr Lys Asp Arg Val Arg Val Pro Leu Ala Tyr Ile Asp Phe Asn
 225 230 235 240
 Ala Tyr Leu Ala Glu Leu Asn Thr Glu Ala Gln Asp Phe Lys Lys Glu
 245 250 255
 Ile Ala Lys Ala Asp Lys Asp Ile Asp Lys Arg Pro Glu Asn Gln Lys
 260 265 270
 Ala Ile Asn Lys Lys Asn Leu Glu Gln Gln Leu Glu Ala Asn Gln
 275 280 285
 Ala Lys Ile Lys Glu Ala Glu Thr Leu Gln Leu Lys His Gly Asp Thr
 290 295 300
 Leu Pro Ile Ser Ala Gly Phe Phe Ile Ile Asn Pro Phe Glu Val Val
 305 310 315 320
 Tyr Tyr Ala Gly Gly Thr Ala Asn Glu Phe Arg His Phe Ala Gly Ser
 325 330 335
 Tyr Ala Val Gln Trp Glu Met Ile Asn Tyr Ala Ile Asp Tyr Gln Ile
 340 345 350
 Pro Arg Tyr Asn Phe Tyr Gly Ile Ser Gly Asp Phe Ser Glu Asp Ala
 355 360 365
 Glu Asp Ala Gly Val Ile Lys Phe Lys Lys Gly Tyr Asn Ala Glu Val
 370 375 380
 Ile Glu Tyr Val Gly Asp Phe Ile Lys Pro Ile Asn Lys Pro Ala Tyr
 385 390 395 400
 Thr Val Tyr Leu Lys Leu Lys Gln Leu Lys Asp Lys Ile Lys Arg
 405 410 415

<210> 50
 <211> 1284
 <212> DNA
 <213> *Staphylococcus sciuri* femA

<220>
 <221> CDS
 <222> (1) ... (1233)

<400> 50
 aca ctg gaa ttt gaa gct ttt aca aat aaa atg ccg tac gcg cat ttt 48
 Thr Leu Glu Phe Glu Ala Phe Thr Asn Lys Met Pro Tyr Ala His Phe
 1 5 10 15
 aca caa gca gta ggt aat tat gaa tta aaa aca tct gaa ggt act tca 96
 Thr Gln Ala Val Gly Asn Tyr Glu Leu Lys Thr Ser Glu Gly Thr Ser
 20 25 30
 aca cat tta gta ggg gtc aaa gat aat caa ggt gaa gta tta gct gcg 144
 Thr His Leu Val Gly Val Lys Asp Asn Gln Gly Glu Val Leu Ala Ala
 35 40 45
 tgt ctg tta aca agt gta cca gtt atg aag aaa ttt aat tac ttt tac 192
 Cys Leu Leu Thr Ser Val Pro Val Met Lys Lys Phe Asn Tyr Phe Tyr
 50 55 60
 tca aat aga gga cca gta atg gat tat gac aac aaa gaa ctt gtt gac 240
 Ser Asn Arg Gly Pro Val Met Asp Tyr Asp Asn Lys Glu Leu Val Asp
 65 70 75 80
 ttt ttc ttt aaa gaa atc gtg agc tat tta aaa agt tat aaa gga tta 288
 Phe Phe Phe Lys Glu Ile Val Ser Tyr Leu Lys Ser Tyr Lys Gly Leu
 85 90 95
 ttc ttt aga atc gat cct tac ttg cca tat caa cta aga gat cat gat 336
 Phe Phe Arg Ile Asp Pro Tyr Leu Pro Tyr Gln Leu Arg Asp His Asp
 100 105 110
 ggc aat att aaa aaa tca ttc aac cgt gat ggt tta att aaa caa ttt 384
 Gly Asn Ile Lys Lys Ser Phe Asn Arg Asp Gly Leu Ile Lys Gln Phe
 115 120 125
 gaa tca tta ggt tat gaa cac caa ggc ttc aca act ggt ttc cac cca 432
 Glu Ser Leu Gly Tyr Glu His Gln Gly Phe Thr Thr Gly Phe His Pro
 130 135 140
 ata cat caa att aga tgg cat tct gta ctt gat tta gaa agt atg gac 480
 Ile His Gln Ile Arg Trp His Ser Val Leu Asp Leu Glu Ser Met Asp
 145 150 155 160
 gaa aag acg ctc atc aag aac atg gac agt tta aga aaa aga aat act 528
 Glu Lys Thr Leu Ile Lys Asn Met Asp Ser Leu Arg Lys Arg Asn Thr
 165 170 175
 aaa aaa gtt caa aaa aat ggt gtt aaa gtt cgt ttt cta tct aaa gat 576
 Lys Lys Val Gln Lys Asn Gly Val Lys Val Arg Phe Leu Ser Lys Asp
 180 185 190
 gaa atg ccg ata ttc cgt caa ttt atg gaa gat act aca gag aag aaa 624
 Glu Met Pro Ile Phe Arg Gln Phe Met Glu Asp Thr Thr Glu Lys Lys
 195 200 205
 gat ttc aac gat cgt ggc gat gac ttc tat tac aat aga tta aaa tac 672
 Asp Phe Asn Asp Arg Gly Asp Asp Phe Tyr Tyr Asn Arg Leu Lys Tyr

210

215

220

ttt gaa aat gta aag att cct tta gca tat ata gac ttt gaa act tac 720
 Phe Glu Asn Val Lys Ile Pro Leu Ala Tyr Ile Asp Phe Glu Thr Tyr
 225 230 235 240

att cca caa tta gaa aaa gaa cat gaa caa tac aac aaa gat att gca 768
 Ile Pro Gln Leu Glu Lys Glu His Glu Gln Tyr Asn Lys Asp Ile Ala
 245 250 255

aaa gct gaa aaa gat tta gaa aag aaa cca gat aat caa aaa acg att 816
 Lys Ala Glu Lys Asp Leu Glu Lys Lys Pro Asp Asn Gln Lys Thr Ile
 260 265 270

aat aaa ata gac aac tta aaa caa caa aga gaa gca aat gaa gct aaa 864
 Asn Lys Ile Asp Asn Leu Lys Gln Gln Arg Glu Ala Asn Glu Ala Lys
 275 280 285

tta gaa gaa gca ctt caa cta caa caa gaa cat ggt gat aca tta cca 912
 Leu Glu Glu Ala Leu Gln Leu Gln Glu His Gly Asp Thr Leu Pro
 290 295 300

ata gca gct ggt ttc ttt att att aat cca ttt gaa gtt gta tat tat 960
 Ile Ala Ala Gly Phe Phe Ile Ile Asn Pro Phe Glu Val Val Tyr Tyr
 305 310 315 320

gca ggt ggt tca tcg aat gaa tat cgt cac ttt gca ggt agt tat gca 1008
 Ala Gly Gly Ser Ser Asn Glu Tyr Arg His Phe Ala Gly Ser Tyr Ala
 325 330 335

att cag tgg gaa atg att aaa tac gcg tta gat cac aac att gac cgt 1056
 Ile Gln Trp Glu Met Ile Lys Tyr Ala Leu Asp His Asn Ile Asp Arg
 340 345 350

tat aac ttc tat ggt atc agc gga gac ttc tca gaa gat gca cct gat 1104
 Tyr Asn Phe Tyr Gly Ile Ser Gly Asp Phe Ser Glu Asp Ala Pro Asp
 355 360 365

gtt ggc gtt att aaa ttt aaa aaa ggt tac aat gca gat gtt tat gaa 1152
 Val Gly Val Ile Lys Phe Lys Lys Gly Tyr Asn Ala Asp Val Tyr Glu
 370 375 380

tat att ggt gat ttc gtt aaa cca att aat aaa cca gcg tac aaa gca 1200
 Tyr Ile Gly Asp Phe Val Lys Pro Ile Asn Lys Pro Ala Tyr Lys Ala
 385 390 395 400

tat aca aca cta aaa aaa gta tta aaa aaa taa atgattttca gtaagagagg 1253
 Tyr Thr Thr Leu Lys Lys Val Leu Lys Lys *
 405 410

aatttagata atatgaaatt tacagagttt a 1284

<210> 51

<211> 410

<212> PRT

<213> Staphylococcus sciuri femA

<400> 51
Thr Leu Glu Phe Glu Ala Phe Thr Asn Lys Met Pro Tyr Ala His Phe
1 5 10 15
Thr Gln Ala Val Gly Asn Tyr Glu Leu Lys Thr Ser Glu Gly Thr Ser
20 25 30
Thr His Leu Val Gly Val Lys Asp Asn Gln Gly Glu Val Leu Ala Ala
35 40 45
Cys Leu Leu Thr Ser Val Pro Val Met Lys Lys Phe Asn Tyr Phe Tyr
50 55 60
Ser Asn Arg Gly Pro Val Met Asp Tyr Asp Asn Lys Glu Leu Val Asp
65 70 75 80
Phe Phe Phe Lys Glu Ile Val Ser Tyr Leu Lys Ser Tyr Lys Gly Leu
85 90 95
Phe Phe Arg Ile Asp Pro Tyr Leu Pro Tyr Gln Leu Arg Asp His Asp
100 105 110
Gly Asn Ile Lys Lys Ser Phe Asn Arg Asp Gly Leu Ile Lys Gln Phe
115 120 125
Glu Ser Leu Gly Tyr Glu His Gln Gly Phe Thr Thr Gly Phe His Pro
130 135 140
Ile His Gln Ile Arg Trp His Ser Val Leu Asp Leu Glu Ser Met Asp
145 150 155 160
Glu Lys Thr Leu Ile Lys Asn Met Asp Ser Leu Arg Lys Arg Asn Thr
165 170 175
Lys Lys Val Gln Lys Asn Gly Val Lys Val Arg Phe Leu Ser Lys Asp
180 185 190
Glu Met Pro Ile Phe Arg Gln Phe Met Glu Asp Thr Thr Glu Lys Lys
195 200 205
Asp Phe Asn Asp Arg Gly Asp Asp Phe Tyr Tyr Asn Arg Leu Lys Tyr
210 215 220
Phe Glu Asn Val Lys Ile Pro Leu Ala Tyr Ile Asp Phe Glu Thr Tyr
225 230 235 240
Ile Pro Gln Leu Glu Lys Glu His Gln Tyr Asn Lys Asp Ile Ala
245 250 255
Lys Ala Glu Lys Asp Leu Glu Lys Lys Pro Asp Asn Gln Lys Thr Ile
260 265 270
Asn Lys Ile Asp Asn Leu Lys Gln Gln Arg Glu Ala Asn Glu Ala Lys
275 280 285
Leu Glu Glu Ala Leu Gln Leu Gln Glu His Gly Asp Thr Leu Pro
290 295 300
Ile Ala Ala Gly Phe Phe Ile Ile Asn Pro Phe Glu Val Val Tyr Tyr
305 310 315 320
Ala Gly Gly Ser Ser Asn Glu Tyr Arg His Phe Ala Gly Ser Tyr Ala
325 330 335
Ile Gln Trp Glu Met Ile Lys Tyr Ala Leu Asp His Asn Ile Asp Arg
340 345 350
Tyr Asn Phe Tyr Gly Ile Ser Gly Asp Phe Ser Glu Asp Ala Pro Asp
355 360 365
Val Gly Val Ile Lys Phe Lys Lys Gly Tyr Asn Ala Asp Val Tyr Glu
370 375 380
Tyr Ile Gly Asp Phe Val Lys Pro Ile Asn Lys Pro Ala Tyr Lys Ala
385 390 395 400
Tyr Thr Thr Leu Lys Lys Val Leu Lys Lys
405 410

<210> 52
 <211> 1343
 <212> DNA
 <213> *Staphylococcus hominis* femA

<220>
 <221> CDS
 <222> (64) ... (1317)

<400> 52
 taaaatttta aaatttagtca actcaaatta aataaaagatt ctaaatttagg agttatagag 60
 ata atg aag ttt aca aat tta aca gct aca gaa ttt ggc gat ttt act 108
 Met Lys Phe Thr Asn Leu Thr Ala Thr Glu Phe Gly Asp Phe Thr
 1 5 10 15

gaa aaa atg cca tat agc cat ttt aca cag atg act gaa aat tat gag 156
 Glu Lys Met Pro Tyr Ser His Phe Thr Gln Met Thr Glu Asn Tyr Glu
 20 25 30

tta aaa gtt gct gag aaa act gaa act cat tta gta gga att aaa aat 204
 Leu Lys Val Ala Glu Lys Thr Glu Thr His Leu Val Gly Ile Lys Asn
 35 40 45

aaa gat aat gaa gtc att gct gct tgt atg cta act gct gta ccc gtt 252
 Lys Asp Asn Glu Val Ile Ala Ala Cys Met Leu Thr Ala Val Pro Val
 50 55 60

atg aaa att ttt aaa tat ttt tat tca aat cgt ggt cca gtc att gat 300
 Met Lys Ile Phe Lys Tyr Phe Tyr Ser Asn Arg Gly Pro Val Ile Asp
 65 70 75

tat gaa aac aaa gaa ctc gtt cac ttt ttc ttt aac gaa tta agt aaa 348
 Tyr Glu Asn Lys Glu Leu Val His Phe Phe Phe Asn Glu Leu Ser Lys
 80 85 90 95

tat tta aaa caa caa cat tgt tta tat gta cgt ata gac cct tat ttg 396
 Tyr Leu Lys Gln Gln His Cys Leu Tyr Val Arg Ile Asp Pro Tyr Leu
 100 105 110

cct tat caa tat cgt aat cat gat ggt gat att aca gga aat gct ggg 444
 Pro Tyr Gln Tyr Arg Asn His Asp Gly Asp Ile Thr Gly Asn Ala Gly
 115 120 125

aat gat tgg ttc ttc gat aaa atg aaa caa tta gga tat caa cac gaa 492
 Asn Asp Trp Phe Phe Asp Lys Met Lys Gln Leu Gly Tyr Gln His Glu
 130 135 140

ggg ttt aca aca gga ttt gat cca ata tta caa att cgg ttc cat tca 540
 Gly Phe Thr Thr Gly Phe Asp Pro Ile Leu Gln Ile Arg Phe His Ser
 145 150 155

gtt tta aat tta aag gat aaa act gct aaa gat gta tta aat gga atg 588
 Val Leu Asn Leu Lys Asp Lys Thr Ala Lys Asp Val Leu Asn Gly Met

160	165	170	175	
gat agt tta cga aaa aga aat act aaa aaa gtc caa aaa aat ggt gtt				636
Asp Ser Leu Arg Lys Arg Asn Thr Lys Lys Val Gln Lys Asn Gly Val				
180		185		190
aaa gta aga ttt ctt act aaa gaa gaa tta cct att ttc aga tca ttt				684
Lys Val Arg Phe Leu Thr Lys Glu Glu Leu Pro Ile Phe Arg Ser Phe				
195		200		205
atg gaa gat aca tca gag act aaa gaa ttt tct gat aga gag gat agt				732
Met Glu Asp Thr Ser Glu Thr Lys Glu Phe Ser Asp Arg Glu Asp Ser				
210		215		220
ttt tac tat aat cga ttt gat cat ttt aaa gat aga gta tta gta cct				780
Phe Tyr Tyr Asn Arg Phe Asp His Phe Lys Asp Arg Val Leu Val Pro				
225		230		235
ctc gca tat ata aaa ttt gat gaa tat ctt gaa gaa ctt cat gca gaa				828
Leu Ala Tyr Ile Lys Phe Asp Glu Tyr Leu Glu Glu Leu His Ala Glu				
240		245		255
cgt cag aca tta aat aaa gac tta aac aaa gct cta aaa gat att gaa				876
Arg Gln Thr Leu Asn Lys Asp Leu Asn Lys Ala Leu Lys Asp Ile Glu				
260		265		270
aaa cga cca gat aac aaa aaa gca caa aat aaa aaa ata aat tta gaa				924
Lys Arg Pro Asp Asn Lys Ala Gln Asn Lys Lys Ile Asn Leu Glu				
275		280		285
cag caa tta aaa gca aat gag caa aaa att gat gaa gca aca caa ctt				972
Gln Gln Leu Lys Ala Asn Glu Gln Lys Ile Asp Glu Ala Thr Gln Leu				
290		295		300
caa tta gaa cat ggt aac gaa tta cca ata tct gct gga ttc ttc ttt				1020
Gln Leu Glu His Gly Asn Glu Leu Pro Ile Ser Ala Gly Phe Phe Phe				
305		310		315
att aat cca ttt gaa gtt gta tat tat gca ggt gga acg tca aat aaa				1068
Ile Asn Pro Phe Glu Val Val Tyr Tyr Ala Gly Gly Thr Ser Asn Lys				
320		325		330
tat aga cac ttc gct gga agt tat gca gtt caa tgg act atg att aat				1116
Tyr Arg His Phe Ala Gly Ser Tyr Ala Val Gln Trp Thr Met Ile Asn				
340		345		350
tat gca att gat cat ggc att gac cgt tat aat ttt tat ggg att agt				1164
Tyr Ala Ile Asp His Gly Ile Asp Arg Tyr Asn Phe Tyr Gly Ile Ser				
355		360		365
ggt cat ttt aca gat gat gct gaa gat gca ggt gtt gta aaa ttt aaa				1212
Gly His Phe Thr Asp Asp Ala Glu Asp Ala Gly Val Val Lys Phe Lys				
370		375		380
aaa gga ttt aat gca gat gta att gaa tat gtt ggt gat ttc gtt aaa				1260

Lys Gly Phe Asn Ala Asp Val Ile Glu Tyr Val Gly Asp Phe Val Lys
 385 390 395
 cct ata aat aaa cca atg tat tca cta tat aca aca ctt aaa aaa att 1308
 Pro Ile Asn Lys Pro Met Tyr Ser Leu Tyr Thr Thr Leu Lys Lys Ile
 400 405 410 415
 aaa aag aga ttgaattaag agggaaatag tgagaa 1343
 Lys Lys Arg

<210> 53
 <211> 418
 <212> PRT
 <213> Staphylococcus hominis femA

D | <400> 53
 Met Lys Phe Thr Asn Leu Thr Ala Thr Glu Phe Gly Asp Phe Thr Glu
 1 5 10 15
 Lys Met Pro Tyr Ser His Phe Thr Gln Met Thr Glu Asn Tyr Glu Leu
 20 25 30
 Lys Val Ala Glu Lys Thr Glu Thr His Leu Val Gly Ile Lys Asn Lys
 35 40 45
 Asp Asn Glu Val Ile Ala Ala Cys Met Leu Thr Ala Val Pro Val Met
 50 55 60
 Lys Ile Phe Lys Tyr Phe Tyr Ser Asn Arg Gly Pro Val Ile Asp Tyr
 65 70 75 80
 Glu Asn Lys Glu Leu Val His Phe Phe Asn Glu Leu Ser Lys Tyr
 85 90 95
 Leu Lys Gln Gln His Cys Leu Tyr Val Arg Ile Asp Pro Tyr Leu Pro
 100 105 110
 Tyr Gln Tyr Arg Asn His Asp Gly Asp Ile Thr Gly Asn Ala Gly Asn
 115 120 125
 Asp Trp Phe Phe Asp Lys Met Lys Gln Leu Gly Tyr Gln His Glu Gly
 130 135 140
 Phe Thr Thr Gly Phe Asp Pro Ile Leu Gln Ile Arg Phe His Ser Val
 145 150 155 160
 Leu Asn Leu Lys Asp Lys Thr Ala Lys Asp Val Leu Asn Gly Met Asp
 165 170 175
 Ser Leu Arg Lys Arg Asn Thr Lys Lys Val Gln Lys Asn Gly Val Lys
 180 185 190
 Val Arg Phe Leu Thr Lys Glu Glu Leu Pro Ile Phe Arg Ser Phe Met
 195 200 205
 Glu Asp Thr Ser Glu Thr Lys Glu Phe Ser Asp Arg Glu Asp Ser Phe
 210 215 220
 Tyr Tyr Asn Arg Phe Asp His Phe Lys Asp Arg Val Leu Val Pro Leu
 225 230 235 240
 Ala Tyr Ile Lys Phe Asp Glu Tyr Leu Glu Glu Leu His Ala Glu Arg
 245 250 255
 Gln Thr Leu Asn Lys Asp Leu Asn Lys Ala Leu Lys Asp Ile Glu Lys
 260 265 270
 Arg Pro Asp Asn Lys Lys Ala Gln Asn Lys Lys Ile Asn Leu Glu Gln
 275 280 285
 Gln Leu Lys Ala Asn Glu Gln Lys Ile Asp Glu Ala Thr Gln Leu Gln

290	295	300
Leu Glu His Gly Asn Glu Leu Pro Ile Ser Ala Gly Phe Phe Ile		
305	310	315
Asn Pro Phe Glu Val Val Tyr Tyr Ala Gly Gly Thr Ser Asn Lys Tyr		320
325	330	335
Arg His Phe Ala Gly Ser Tyr Ala Val Gln Trp Thr Met Ile Asn Tyr		
340	345	350
Ala Ile Asp His Gly Ile Asp Arg Tyr Asn Phe Tyr Gly Ile Ser Gly		
355	360	365
His Phe Thr Asp Asp Ala Glu Asp Ala Gly Val Val Lys Phe Lys Lys		
370	375	380
Gly Phe Asn Ala Asp Val Ile Glu Tyr Val Gly Asp Phe Val Lys Pro		
385	390	395
Ile Asn Lys Pro Met Tyr Ser Leu Tyr Thr Thr Leu Lys Lys Ile Lys		400
405	410	415
Lys Arg		

D
 <210> 54
 <211> 2742
 <212> DNA
 <213> *Staphylococcus saprophyticus* femA

<220>
 <221> CDS
 <222> (64)...(1326)

<400> 54
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 aaa atg aaa ttt acg aat tta act gca aaa gag ttc ggt gca ttt acg 108
 Met Lys Phe Thr Asn Leu Thr Ala Lys Glu Phe Gly Ala Phe Thr
 1 5 10 15

gat aaa atg ccg aat agt cat ttt acg caa atg gtt gga aat tat gaa 156
 Asp Lys Met Pro Asn Ser His Phe Thr Gln Met Val Gly Asn Tyr Glu
 20 25 30

ttg aaa att gca gaa agt aca gaa aca cac cta gta ggt att aag aat 204
 Leu Lys Ile Ala Glu Ser Thr Glu Thr His Leu Val Gly Ile Lys Asn
 35 40 45

aat gat aat gaa gta att gca gca tgt tta ctt aca gct gtt cct gtt 252
 Asn Asp Asn Glu Val Ile Ala Ala Cys Leu Leu Thr Ala Val Pro Val
 50 55 60

atg aaa ttc ttc aag tat ttt tat tcc aat aga ggt cca gtc ata gat 300
 Met Lys Phe Phe Lys Tyr Phe Tyr Ser Asn Arg Gly Pro Val Ile Asp
 65 70 75

ttt gaa aat aaa gaa ctc gta cat tac ttc ttt aac gaa tta gca aaa 348
 Phe Glu Asn Lys Glu Leu Val His Tyr Phe Phe Asn Glu Leu Ala Lys
 80 85 90 95

tat gta aaa aaa cat aat gcc tta tat tta cga gta gat cct tat ctt 396

Tyr Val Lys Lys His Asn Ala Leu Tyr Leu Arg Val Asp Pro Tyr Leu
 100 105 110
 gct tat caa tat cgt aat cat gat ggt gaa gta tta gca aat gcg ggt 444
 Ala Tyr Gln Tyr Arg Asn His Asp Gly Glu Val Leu Ala Asn Ala Gly
 115 120 125
 cac gat tgg att ttt gat aaa atg aaa caa ctc ggt tat aag cat gaa 492
 His Asp Trp Ile Phe Asp Lys Met Lys Gln Leu Gly Tyr Lys His Glu
 130 135 140
 ggt ttt tta act ggc ttt gac cca ata ctt caa ata aga ttc cat tct 540
 Gly Phe Leu Thr Gly Phe Asp Pro Ile Leu Gln Ile Arg Phe His Ser
 145 150 155
 gtt tta gat tta gct gga aaa act gct aaa gac gta ctt aat ggt atg 588
 Val Leu Asp Leu Ala Gly Lys Thr Ala Lys Asp Val Leu Asn Gly Met
 160 165 170 175
 gat agt tta cgt aaa cga aat act aaa aaa gta cag aaa aat ggt gtg 636
 Asp Ser Leu Arg Lys Arg Asn Thr Lys Lys Val Gln Lys Asn Gly Val
 180 185 190
 D) aaa gta aga ttt tta ggt gaa gat gag ttg cca ata ttc cgc tca ttc 684
 Lys Val Arg Phe Leu Gly Glu Asp Glu Leu Pro Ile Phe Arg Ser Phe
 195 200 205
 atg gaa gat act tct gaa aca aag gat ttt gac gat aga gat gac gat 732
 Met Glu Asp Thr Ser Glu Thr Lys Asp Phe Asp Asp Arg Asp Asp Asp
 210 215 220
 ttt tat tat aat agg tta aga tat tat aaa gat cgt gtg ctt gtc cca 780
 Phe Tyr Tyr Asn Arg Leu Arg Tyr Tyr Lys Asp Arg Val Leu Val Pro
 225 230 235
 tta gct tat atg gat ttt gat gaa tat ata aca gaa tta aag gct gaa 828
 Leu Ala Tyr Met Asp Phe Asp Glu Tyr Ile Thr Glu Leu Lys Ala Glu
 240 245 250 255
 cgc gaa gta tta agt aaa gat ata aat aaa gca gtt aag gat ata gaa 876
 Arg Glu Val Leu Ser Lys Asp Ile Asn Lys Ala Val Lys Asp Ile Glu
 260 265 270
 aaa aga cca gaa aat aaa aaa gcg tat aat aaa aaa gaa aat tta gaa 924
 Lys Arg Pro Glu Asn Lys Lys Ala Tyr Asn Lys Lys Glu Asn Leu Glu
 275 280 285
 caa caa ctg att gca aac caa caa aaa ata gat gaa gcc act gcg tta 972
 Gln Gln Leu Ile Ala Asn Gln Gln Lys Ile Asp Glu Ala Thr Ala Leu
 290 295 300
 caa gag aag cat ggt aac gaa tta ccg att tct gca gct tac ttt att 1020
 Gln Glu Lys His Gly Asn Glu Leu Pro Ile Ser Ala Ala Tyr Phe Ile
 305 310 315

att aat cct tat gaa gtc gtt tac tat gca ggt ggt aca tct aat gaa 1068
 Ile Asn Pro Tyr Glu Val Val Tyr Tyr Ala Gly Gly Thr Ser Asn Glu
 320 325 330 335

 ttt aga cat ttt gct ggt agt tat gca ata caa tgg aag atg att aat 1116
 Phe Arg His Phe Ala Gly Ser Tyr Ala Gln Trp Lys Met Ile Asn
 340 345 350

 tat gct ata gat cat aat ata gat aga tat aat ttt tat ggt att agt 1164
 Tyr Ala Ile Asp His Asn Ile Asp Arg Tyr Asn Phe Tyr Gly Ile Ser
 355 360 365

 ggt cat ttt act gaa gat gca gaa gat gca ggt gtt gtt aaa ttt aaa 1212
 Gly His Phe Thr Glu Asp Ala Glu Asp Ala Gly Val Val Lys Phe Lys
 370 375 380

 aaa ggt ttt aat gca gat gta gta gaa tat gtt ggt gat ttt att aaa 1260
 Lys Gly Phe Asn Ala Asp Val Val Glu Tyr Val Gly Asp Phe Ile Lys
 385 390 395

 ccg att aat aag cca atg tac aaa att tat acg aca ttg aaa aaa att 1308
 Pro Ile Asn Lys Pro Met Tyr Lys Ile Tyr Thr Thr Leu Lys Lys Ile
 400 405 410 415

 aag gat aaa aag aaa taa acataaatag aaggaaacta agctagaatg 1356
 Lys Asp Lys Lys Lys *
 420

 aaatttacag agttaacttg ttttagattag aattaaactc gaaaatagaa ctataataa 1416
 ataggagtag ataaaaaaat gaaatttacg aatttaactg caaaagagtt cggcgttattt 1476
 acggataaaa tgccaaatag tcattttacg caaatggttg gaaattatga attgaaaatt 1536
 gcagaaatgtc cagaaacaca ccttagtagt attaagaata atgataatga agtaattgca 1596
 gcatgtttac ttacagctgt tcctgttatg aaatttctca agtatttttta ttccaaataga 1656
 ggtccagtc tagattttga aaataaaagaa ctcgtacatt acttctttaa cgaatttagca 1716
 aaatatgtaa aaaaacataa tgccattat tatcagtagtag atccttatct tgcttatcaa 1776
 tatcgtaatc atgatggta agtattagca aatgcgggtc acgattggat ttttgataaaa 1836
 atgaaacaac tcggttataa gcatgaaggt tttttaactg gcttgcaccc aataacttcaa 1896
 ataagattcc attctgtttt agatttagct ggaaaaactg ctaaagacgt acttaatgg 1956
 atggatagtt tacgtaaacg aaatactaaa aaagtacaga aaaatgggt gaaagtaaga 2016
 tttttaggtg aagatgagtt gccaatattc cgctcattca tggaagatac ttctgaaaca 2076
 aaggattttg acgatagaga tgacgattt tattataata ggttaagata ttataaagat 2136
 cgtgtgtttc tccatttgc ttatatgtat tttgtatgaat atataacaga attaaaggct 2196
 gaacgcgaag tattaaatgaa agatataat aaagcagtta aggatataaa aaaaagacca 2256
 gaaaataaaa aagcgtataa taaaaaaagaa aatttagaaac aacaactgtat tgccaaaccaa 2316
 caaaaaatgtc atgaagccac tgcgttacaa gagaagcatg gtaacgaatt accgatttct 2376
 gcagcttact ttattattaa tccttatgaa gtcgttact atgcagggtg tacatcta 2436
 gaatttagac attttgcgttgg tagttatgca atacaatggaa agatgattaa ttatgctata 2496
 gatcataata tagatagata taatttttattt ggtatttagt gtcattttac tgaagatgca 2556
 gaagatgcag gtgtgtttaa attaaaaaaa ggtttatg cagatgtatg agaatatgtt 2616
 ggtgatttttta taaaaccgat taataaggca atgtacaaaaa ttatagcactt attgaaaaaa 2676
 attaaggata aaaagaaata aacataaaata gaaggaaact aagctagaat gaaattttaca 2736
 gaggta 2742

<210> 55
 <211> 420

<212> PRT

<213> Staphylococcus saprophyticus femA

<400> 55

Met Lys Phe Thr Asn Leu Thr Ala Lys Glu Phe Gly Ala Phe Thr Asp
1 5 10 15
Lys Met Pro Asn Ser His Phe Thr Gln Met Val Gly Asn Tyr Glu Leu
20 25 30
Lys Ile Ala Glu Ser Thr Glu Thr His Leu Val Gly Ile Lys Asn Asn
35 40 45
Asp Asn Glu Val Ile Ala Ala Cys Leu Leu Thr Ala Val Pro Val Met
50 55 60
Lys Phe Phe Lys Tyr Phe Tyr Ser Asn Arg Gly Pro Val Ile Asp Phe
65 70 75 80
Glu Asn Lys Glu Leu Val His Tyr Phe Phe Asn Glu Leu Ala Lys Tyr
85 90 95
Val Lys Lys His Asn Ala Leu Tyr Leu Arg Val Asp Pro Tyr Leu Ala
100 105 110
Tyr Gln Tyr Arg Asn His Asp Gly Glu Val Leu Ala Asn Ala Gly His
115 120 125
Asp Trp Ile Phe Asp Lys Met Lys Gln Leu Gly Tyr Lys His Glu Gly
130 135 140
Phe Leu Thr Gly Phe Asp Pro Ile Leu Gln Ile Arg Phe His Ser Val
145 150 155 160
Leu Asp Leu Ala Gly Lys Thr Ala Lys Asp Val Leu Asn Gly Met Asp
165 170 175
Ser Leu Arg Lys Arg Asn Thr Lys Lys Val Gln Lys Asn Gly Val Lys
180 185 190
Val Arg Phe Leu Gly Glu Asp Glu Leu Pro Ile Phe Arg Ser Phe Met
195 200 205
Glu Asp Thr Ser Glu Thr Lys Asp Phe Asp Asp Arg Asp Asp Asp Phe
210 215 220
Tyr Tyr Asn Arg Leu Arg Tyr Tyr Lys Asp Arg Val Leu Val Pro Leu
225 230 235 240
Ala Tyr Met Asp Phe Asp Glu Tyr Ile Thr Glu Leu Lys Ala Glu Arg
245 250 255
Glu Val Leu Ser Lys Asp Ile Asn Lys Ala Val Lys Asp Ile Glu Lys
260 265 270
Arg Pro Glu Asn Lys Lys Ala Tyr Asn Lys Lys Glu Asn Leu Glu Gln
275 280 285
Gln Leu Ile Ala Asn Gln Gln Ile Asp Glu Ala Thr Ala Leu Gln
290 295 300
Glu Lys His Gly Asn Glu Leu Pro Ile Ser Ala Ala Tyr Phe Ile Ile
305 310 315 320
Asn Pro Tyr Glu Val Val Tyr Tyr Ala Gly Gly Thr Ser Asn Glu Phe
325 330 335
Arg His Phe Ala Gly Ser Tyr Ala Ile Gln Trp Lys Met Ile Asn Tyr
340 345 350
Ala Ile Asp His Asn Ile Asp Arg Tyr Asn Phe Tyr Gly Ile Ser Gly
355 360 365
His Phe Thr Glu Asp Ala Glu Asp Ala Gly Val Val Lys Phe Lys Lys
370 375 380
Gly Phe Asn Ala Asp Val Val Glu Tyr Val Gly Asp Phe Ile Lys Pro
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405

410

415

Asp Lys Lys Lys
420

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